

FIG. 1A

9	18	27	36	45	54
NGG GGG GCG TAC GGA GGT GGC AGC TGT GGG AGG AGG CGT GGA AGG CCG AGG					
63	72	81	90	99	108
AGC TCA AGC CCG GAC CAA TCC CCA CGT TCC GGG CCG CCA CCC TGA CCC TGC AGC					
117	126	135	144	153	162
GTA CCG GGA AGC GAA ACC GGC CGG ATG GGC CGC TGA GCC CGA ATC GGG CAC TGT					
171	180	189	198	207	216
GTG GAG CCC CCT GGA GCT GAG ATC AGG ATG TTC CGC TTC ATG AGG GAC GTG GAG					
		M	F	R	F
225	234	243	252	261	270
CCT GAG GAT CCC ATG TTC CTG ATG GAT CCC TTT GCT ATT CAC CGT CAG CAT ATG					
P	E	D	P	F	A
279	288	297	306	315	324
AGC CGT ATG TTG TCA GGT GGC GGC TTT GGA TAT AGC CCC TTC CTC AGC ATC ACA GAT					
S	R	M	L	S	G
333	342	351	360	369	378
GGC AAC ATG CCA GGG ACC AGG GCT GCC AGC CGC CGG ATG CAG CAG GCT GGA GCT					
G	N	M	P	G	T
387	396	405	414	423	432
GTC TNC CCC TTT GGG NTG CTG GGA ATG TCG GGT GGT TTC ATG GAC ATG TTT GGG					
V	X	P	F	G	X

FIGURE 1A

TTTTTGGGGGG

441	450	459	468	477	486
ATG ATG AAT GAC ATG NTT GGA AAC ATG GAA CAC ATG ACA GCT GGA GGC AAT TGC					
M M N D M X G N M E H M T A G G N C					
495	504	513	522	531	540
CAG ACC TTC TCA TCT TCC ACT GTC ATC TCC TAC TCC AAT ACG GGT GAT GGT GCC					
Q T F S S S T V I S Y S N T G D G A					
549	558	567	576	585	594
CCC AAG GTC TAC CAA GAG ACA TCA GAG ATG CGC TCG GCA CCA GGC GGG ATC CGG					
P K V Y Q E T S E M R S A P G G I R					
603	612	621	630	639	648
GAG ACA CGG AGG ACT GTT CGG GAT TCA GAC AGT GGA CTG GAG CAG ATG TCC ATT					
E T R R T V R D S D S G L E Q M S I					
657	666	675	684	693	702
GGG CAT CAC ATC CGG GAC AGG GCT CAC ATC CTC CAG CGC TCC CGA AAC CAT CGC					
G H H I R D R A H I L Q R S R N H R					
711	720	729	738	747	756
ACG GGG GAC CAG GAG GAG CGG CAG GAC TAT ATC AAC CTG GAT GAG AGT GAG GCC					
T G D Q E E R Q D Y I N L D E S E A					
765	774	783	792	801	810
GCA GCG TTT GAT GAC GAG TGG CGG CGG GAG ACC TCC CGA TTC CGG CAG CAG CGT					
A A F D D E W R R E T S R F R Q Q R					

FIGURE 1B

TTTTGGGGGG

819	828	837	846	855	864
CCC CTG GAG TTT CGG CGG CTT GAG TCC TCA GGG GCT GGG CGA AGG GCG GAG					
P L E F R R R L E S S S G A G G R A E					
873	882	891	900	909	918
GGG CCT CCC CGC CTG GCC ATC CAG GGA CCT GAG GAC TCC CTT CCC GAC AGT CCC					
G P P R L A I Q G G P E D S L P D S P					
927	936	945	954	963	972
GCC GCT ATG ACT GGT GAG GGC CCC GGG GCC TCA GCT CTC TTG TAC AGG CTG AGA					
A A M T G E G P G A S A L L Y R L R					
981	990	999	1008	1017	1026
GGC TGA GAA ATC ATC CCC TGA ATA ACT TTT TCC TCT CGA TTC CCA TCC CCA ATT					
G * E I I P * I T F S S R F P S P I					
1035	1044	1053	1062	1071	1080
TAA TAT TAA ATT AAC AGG CAA GCC GGC CCC CAC CTC TCC CTG GGG GTC TCA GGG					
* Y * I N R Q A G P H L S L G V S G					
1089	1098	1107	1116	1125	1134
AGA ACC TTT CAC GGC ACC CTT TCC CTA CCT TTT CCT TCT TTA ATC TCC TGG TTT					
R T F H G T L S L P F P S S L I S W F					
1143	1152	1161	1170	1179	1188
ACC ATT GAT GAC TTC GGC TCT GCA TCT ACT TAC TTG ATT TTT CAT TCT GCC ACT					
T I D D F G S A S T Y L I F H S A T					

FIGURE 1C

1197	1206	1215	1224	1233	1242
TCA TCT TCA AAC CCC CTC ACC TTT CCC ATC CTA CTC CTG CCA TGC ATT GAA GGG					
S S S N P L T F P I L L L L P C I E G					
1251	1260	1269	1278	1287	1296
TCA ATG CAT TTT GGG GTG AGN TTN GGT TTA GGG GCC CCT TCA TNC CTN AGC TAC					
S M H F G V X X G L G A P S X L S Y					
1305	1314	1323			
CTG GGT CTT TGC CCA ACT TTT CTC AGA					
L G L C P T F L R					

FIGURE 1D

TABLE 1

1	M	F	R	F	M	R	D	V	E	P	E	D	P	M	F	L	M	D	P	F	A	I	H	R	Q	H	M	S	R	M	762280	
1	M	F	R	M	L	N	S	S	F	E	D	D	P	-	F	F	S	E	S	I	L	A	H	R	E	N	M	R	Q	M	GI 1066392	
1	M	F	R	F	M	R	D	V	E	P	E	D	P	M	F	L	M	D	P	F	A	I	H	R	Q	H	M	S	R	M	GI 1399745	
31	L	-	-	-	S	G	G	F	G	Y	S	P	F	L	S	I	T	D	G	N	M	P	G	T	R	A	A	S	R	R	762280	
30	I	R	S	F	S	E	P	F	G	-	R	D	L	L	S	I	S	D	G	R	-	-	G	R	A	H	N	R	R	GI 1066392		
31	L	-	-	-	S	G	G	F	G	Y	S	P	F	L	S	I	T	D	G	N	M	P	G	T	R	P	A	S	R	R	GI 1399745	
58	M	Q	Q	A	G	A	-	-	-	-	-	-	-	-	V	X	P	F	G	X	L	G	M	S	G	G	F	M	D	M	F	762280
56	G	H	N	D	G	E	D	S	L	T	H	T	D	V	S	S	F	Q	T	M	D	Q	M	V	S	N	M	R	N	Y	GI 1066392	
58	M	Q	Q	A	G	A	-	-	-	-	-	-	-	-	V	S	P	F	G	M	L	G	M	S	G	G	F	M	D	M	F	GI 1399745
81	G	M	M	N	D	M	X	G	N	M	E	H	M	T	A	G	G	N	C	Q	T	F	S	S	S	T	V	I	S	Y	762280	
86	-	-	M	Q	K	L	E	R	N	F	G	Q	L	S	V	D	P	N	G	H	S	F	C	S	S	S	V	M	T	Y	GI 1066392	
81	G	M	M	N	D	M	I	G	N	M	E	H	M	T	A	G	G	N	C	Q	T	F	S	S	S	T	V	I	S	Y	GI 1399745	
111	S	N	T	G	D	G	A	P	K	V	Y	Q	E	T	S	E	M	R	S	A	P	G	G	I	R	E	T	R	R	T	762280	
114	S	K	I	G	D	E	P	P	K	V	F	Q	A	S	T	Q	T	R	R	A	P	G	G	I	K	E	T	R	K	A	GI 1066392	
111	S	N	T	G	D	G	A	P	K	V	Y	Q	E	T	S	E	M	R	S	A	P	G	G	I	R	E	T	R	R	T	GI 1399745	
141	V	R	D	S	D	S	G	L	E	Q	M	S	I	G	H	H	I	R	D	R	A	H	I	L	Q	R	S	R	N	H	762280	
144	M	R	D	S	D	S	G	L	E	K	M	A	I	G	H	H	I	H	D	R	A	H	V	I	K	K	S	K	N	K	GI 1066392	
141	V	R	D	S	D	S	G	L	E	Q	M	S	I	G	H	H	I	R	D	R	A	H	I	L	Q	R	S	R	N	H	GI 1399745	

FIGURE 2A

171	R T G D Q E E R Q D Y I N L D E S E A A F D D E W R R E T	762280
174	K T G D E E V N Q E F I N M N E S D A H A F D E E W Q S E V	GI 1066392
171	R T G D Q E E R Q D Y I N L D E S E A A F D D E W R R E T	GI 1399745
201	S R F R Q Q R P - L E F R R L E S S G A G - - G R R A E G P	762280
204	L K Y K P G R H N L G N T R M R S V G H E N P G S R E L K R	GI 1066392
201	S R F R Q Q R P - L E F R R L E S S G A G - - G R R A E G P	GI 1399745
228	P R L A I Q G P E D S L P D S P A A M T G E G P G A S A L L	762280
234	R E K P Q Q S P A I E H G R R S N V L G D K L H I K G S S V	GI 1066392
228	P R L A I Q G P E D S - - - - - P S R Q S R R	GI 1399745
258	Y R L R G	762280
264	K S N K K	GI 1066392
246	Y D W	GI 1399745

FIGURE 2B

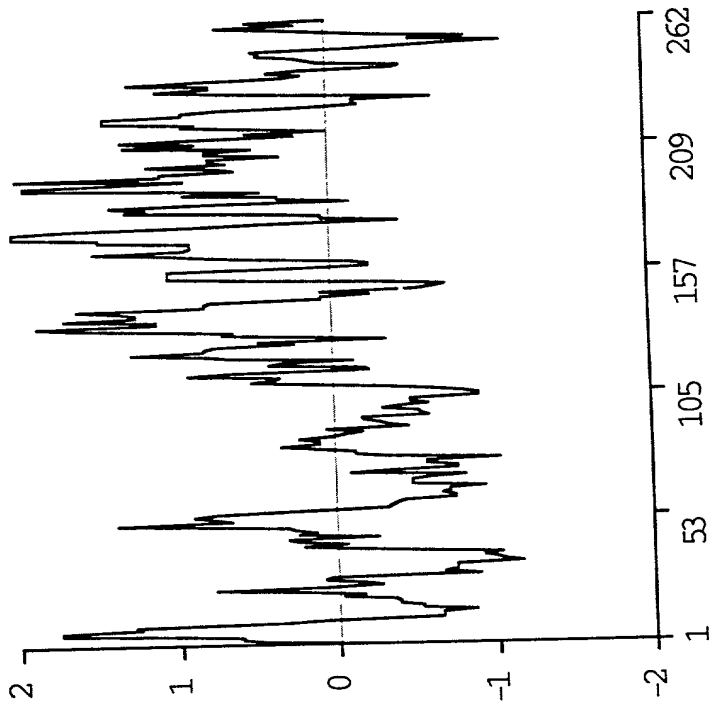


FIGURE 3A

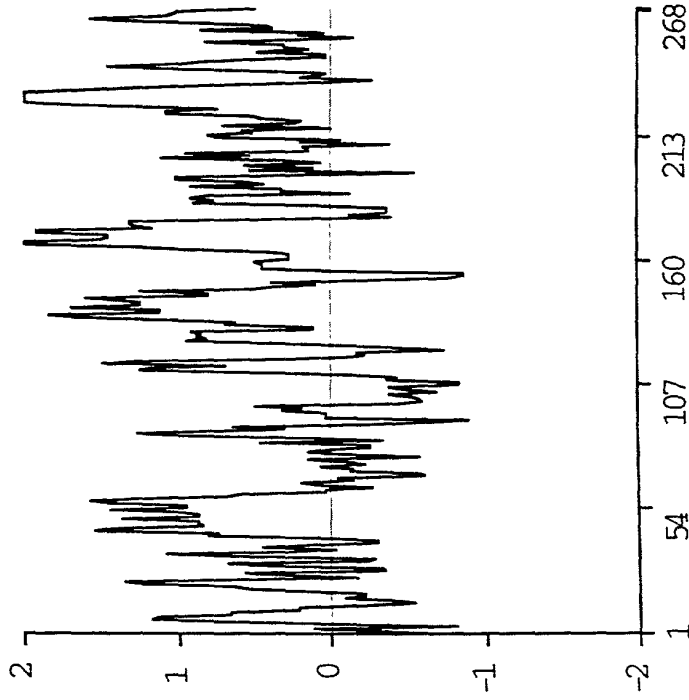


FIGURE 3B

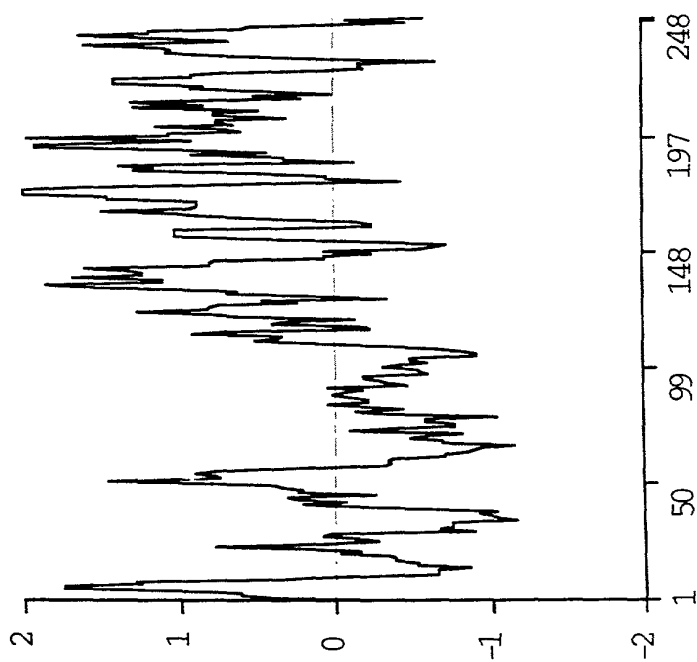


FIGURE 3C

Library	Lib Description	Abun	Pct Abun
BRAINOT11	brain, right temporal, epilepsy, 5 M	4	0.1289
PITUNOT03	pituitary, 46 M	3	0.1045
BRAINOM02	brain, 55 M, NORM, WM	2	0.0907
PGANNOT03	paraganglionic tumor, 46 M	2	0.0622
STOMNOT02	stomach, 52 M, match to STOMTUT01	2	0.0615
BRAINOT12	brain, right frontal, epilepsy, 5 M	2	0.0607
PROSNOT05	prostate, 67 M, match to PROSTUT03	1	0.0576
HNT3AZT01	hNT2 cell line, treated AZ	3	0.0572
BMARNOT03	bone marrow, 16 M	2	0.0484
BRSTNOT03	breast, 54 F, match to BRSTTUT	3	0.0441
STOMTUT01	stomach tumor, 52 M,	1	0.0368
BRAINOT04	brain, choroid plexus, 44 M	1	0.0356
BRAINOT10	brain, cerebellum, Alzheimer's, 74 M	1	0.0348
HNT2NOT01	hNT2 cell line, control	2	0.0345
MMLR3DT01	macrophages (adher PBMNC), 72-hr MLR	1	0.0332
SPLNFEM01	spleen, fetal, WM	1	0.0332
BRAINOT14	brain, 40 F, match BRAITUT12	1	0.0315
NEUTGMT01	granulocytes, M/F, treated GM-CSF	2	0.0313
THYRNOT02	thyroid, hyperthyroidism, 16 F	1	0.0303
BRAINON01	brain, 26 M, NORM	3	0.0296
TONGTUT01	tongue tumor, carcinoma, 36 M	1	0.0295
BRAITUT08	brain tumor, astrocytoma, 47 M	2	0.0293
BEPINOT01	bronchial epithelium, 54 M	2	0.0289
FIBRSEM01	fibroblasts, senescent, NORM, WM	1	0.0289
COLNNOT05	colon, 40 M, match to COLNCRT01	1	0.0289
STOMTUT02	stomach tumor, lymphoma, 68 F	1	0.0284
PROSNOT11	prostate, 28 M	1	0.0282
BRSTTUT02	breast tumor, 54 F, match BRSTNOT03	2	0.0279
BLADNOT04	bladder and seminal vesicle, 28 M	1	0.0278
UTRSNOT05	uterus, 45 F	1	0.0278
PROSNOT19	prostate, 59 M	1	0.0272
BRAINOM03	brain, 55 M, NORM, WM	1	0.0270
ENDCNOT01	endothelial cells, coronary artery, 58 M	1	0.0268
KIDNTUT01	kidney tumor, Wilms, 8m F	1	0.0267
PENITUT01	penis tumor, carcinoma, 64 M	1	0.0267
LNODNOT03	lymph node, 67 M	1	0.0265
LEUKNOT03	white blood cells, 27 F	1	0.0262
URETTUT01	ureter tumor, 69 M	1	0.0262
ENDANOT01	endothelial cells, aorta, M	2	0.0257
PROSNOT18	prostate, 58 M	1	0.0256
BRSTTUT08	breast tumor, 45 F, match to BRSTNOT09	1	0.0254
SPLNFET02	spleen, fetal M	2	0.0252
UTRSNOT02	uterus, 34 F	3	0.0233
PROSNOT06	prostate, 57 M, match to PROSTUT04	2	0.0229
NERVMSM01	multiple sclerosis, 46 M, NORM, WM	1	0.0224
ENDCNOT03	endothelial cells, neonatal M	1	0.0210
OVARTUT01	ovarian tumor, 43 F	2	0.0207
UTRPNOM01	uterus, F, NORM, WM	1	0.0201
LUNGNOT03	lung, 79 M, match to LUNGTUT02	1	0.0200

FIGURE 4A

BRSTNOT04	breast, 62 F	2	0.0192
BRSTTUT01	breast tumor, 55 F, match BRSTNOT02	2	0.0189
HNT2RAT01	hNT2 cell line, treated RA	1	0.0188
BRAINOT09	brain, fetal M	2	0.0186
SYNOOAT01	synovium, knee, osteoarthritis, 82 F	1	0.0180
MMLR2DT01	macrophages (adher PBMC), 48-hr MLR	1	0.0178
SINTBST01	small intestine, ileum, Crohn's, 18 F	1	0.0168
PGANNOAT01	paraganglionic tumor, 46 M	1	0.0160
BRSTNOT05	breast, 58 F, match to BRSTTUT03	2	0.0149
CONNNOT01	fat, mesentery, 71 M	1	0.0149
BRSTNOT07	breast, 43 F	1	0.0146
NGANNOAT01	ganglioneuroma, 9 M	2	0.0146
COLNFET02	colon, fetal F	1	0.0143
LUNGFET03	lung, fetal F	2	0.0138
THYRNOT03	thyroid tumor, adenoma, 28 F	1	0.0138
LATRTUT02	heart tumor, myoma, 43 M	1	0.0137
PITUNOT02	pituitary, 15-75 M/F	1	0.0135
BRAINOM01	brain, infant F, NORM, WM	3	0.0134
PROSNOT16	prostate, 68 M	1	0.0132
CONUTUT01	mesentery tumor, sigmoid, 61 F	1	0.0130
BLADTUT04	bladder tumor, 60 M, match BLADNOT05	1	0.0127
PROSTUT04	prostate tumor, 57 M, match PROSNOT06	1	0.0117
KIDNNOT05	kidney, neonatal F	1	0.0106
MELANOM01	melanocytes, M, NORM, WM	1	0.0096
PROSNON01	prostate, 28 M, NORM	1	0.0094
BRAITUT02	brain tumor, metastasis, 58 M	1	0.0075
ISLTNOT01	pancreas, islet cells, M/F	1	0.0064
LIVSFEM02	liver/spleen, fetal M, NORM, WM	2	0.0053

FIGURE 4B